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SEQUENCE LISTING

<110> Garvan Institute of Medical Research  
<120> Method of modulating bone growth, remodeling and adiposity  
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<160> 20  
<170> PatentIn version 3.3  
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gcc ttt gcc gtg ctc tgg ctg cct ctg cat gtg ttc aac agc ctg gaa		1523
Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Ser Leu Glu		
275 280 285		
gac tgg cac cat gag gcc atc ccc atc tgc cac ggg aac ctc atc ttc		1571
Asp Trp His His Glu Ala Ile Pro Ile Cys His Gly Asn Leu Ile Phe		
290 295 300		
tta gtg tgc cac ttg ctt gcc atg gcc tcc acc tgc gtc aac cca ttc		1619
Leu Val Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe		
305 310 315 320		
atc tat ggc ttt ctc aac acc aac ttc aag aag gag atc aag gcc ctg		1667
Ile Tyr Gly Phe Leu Asn Thr Asn Phe Lys Lys Glu Ile Lys Ala Leu		
325 330 335		
gtg ctg act tgc cag cag agc gcc ccc ctg gag gag tcg gag cat ctg		1715
Val Leu Thr Cys Gln Gln Ser Ala Pro Leu Glu Glu Ser Glu His Leu		
340 345 350		
ccc ctg tcc aca gta cat acg gaa gtc tcc aaa ggg tcc ctg agg cta		1763
Pro Leu Ser Thr Val His Thr Glu Val Ser Lys Gly Ser Leu Arg Leu		
355 360 365		
agt ggc agg tcc aat ccc att taa ccaggtcttag gtcttctccc tgccatgtcc		1817
Ser Gly Arg Ser Asn Pro Ile		
370 375		
cttgccaggc tcttccactt agctaagtgg gcacactgca agctgggtg gcacccccc		1877
atccctggct ttctgggtc cagataggct ggcaagagct gttttgcat ccatttgcatt		1937

cgtgaagact ggcattttga tacttcagct gtttggcctt gggagaattc tgagcacaga	1997
ttccagaggt cacagtaagc cttgcagctt gagctgaaag atgccagagc cgaggatgtc	2057
tgctggcagc aggcagggtt cattctggtg acacagcaac agatccctgg cctggaaacc	2117
cagggatttc acctccacca gtgagaccac ggggccactg tggggtgagg gaaggagcgc	2177
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 20 25 30

His Cys Gln Asp Ser Val Asp Val Met Val Phe Ile Val Thr Ser Tyr  
           35                40                          45

Ser Ile Glu Thr Val Val Gly Val Leu Gly Asn Leu Cys Leu Met Cys  
50 55 60

Val Thr Val Arg Gln Lys Glu Lys Ala Asn Val Thr Asn Leu Leu Ile  
65 70 75 80

Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Leu Cys Gln Pro  
85 90 95

Leu Thr Ala Val Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Thr  
           100                 105                 110

Leu Cys Lys Met Ser Ala Phe Ile Gln Cys Met Ser Val Thr Val Ser  
115 120 125

Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile  
130 135 140

Asn	Pro	Thr	Gly	Trp	Lys	Pro	Ser	Ile	Ser	Gln	Ala	Tyr	Leu	Gly	Ile
145					150					155					160

Val Leu Ile Trp Val Ile Ala Cys Val Leu Ser Leu Pro Phe Leu Ala  
165 170 175

Asn Ser Ile Leu Glu Asn Val Phe His Lys Asn His Ser Lys Ala Leu  
180 185 190

Glu Phe Leu Ala Asp Lys Val Val Cys Thr Glu Ser Trp Pro Leu Ala  
195 200 205

His His Arg Thr Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys  
210 215 220

Leu Pro Leu Gly Phe Ile Leu Val Cys Tyr Ala Arg Ile Tyr Arg Arg  
225 230 235 240

Leu Gln Arg Gln Gly Arg Val Phe His Lys Gly Thr Tyr Ser Leu Arg  
245 250 255

Ala Gly His Met Lys Gln Val Asn Val Val Leu Val Val Met Val Val  
260 265 270

Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Ser Leu Glu  
275 280 285

Asp Trp His His Glu Ala Ile Pro Ile Cys His Gly Asn Leu Ile Phe  
290 295 300

Leu Val Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe  
305 310 315 320

Ile Tyr Gly Phe Leu Asn Thr Asn Phe Lys Lys Glu Ile Lys Ala Leu  
325 330 335

Val Leu Thr Cys Gln Gln Ser Ala Pro Leu Glu Glu Ser Glu His Leu  
340 345 350

Pro Leu Ser Thr Val His Thr Glu Val Ser Lys Gly Ser Leu Arg Leu  
355 360 365

Ser Gly Arg Ser Asn Pro Ile  
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agactataat atg gat tta gag ctc gac gag tat tat aac aag aca ctt 109  
Met Asp Leu Glu Leu Asp Glu Tyr Tyr Asn Lys Thr Leu  
1 5 10

gcc aca gag aat aat act gct gcc act cgg aat tct gat ttc cca gtc 157  
Ala Thr Glu Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val  
15 20 25

tgg gat gac tat aaa agc agt gta gat gac tta cag tat ttt ctg att 205  
Trp Asp Asp Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile  
30 35 40 45

ggg ctc tat aca ttt gta agt ctt ctt ggc ttt atg ggg aat cta ctt 253  
Gly Leu Tyr Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu  
50 55 60

att tta atg gct ctc atg aaa aag cgt aat cag aag act acg gta aac 301  
Ile Leu Met Ala Leu Met Lys Lys Arg Asn Gln Lys Thr Thr Val Asn  
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ttc ctc ata ggc aat ctg gcc ttt tct gat atc ttg gtt gtg ctg ttt 349  
Phe Leu Ile Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe  
80 85 90

tgc tca cct ttc aca ctg acg tct gtc ttg ctg gat cag tgg atg ttt 397  
Cys Ser Pro Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe  
95 100 105

ggc aaa gtc atg tgc cat att atg cct ttt ctt caa tgt gtg tca gtt 445  
Gly Lys Val Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val  
110 115 120 125

ttg gtt tca act tta att tta ata tca att gcc att gtc agg tat cat 493  
Leu Val Ser Thr Leu Ile Leu Ser Ile Ala Ile Val Arg Tyr His  
130 135 140

atg ata aaa cat ccc ata tct aat aat tta aca gca aac cat ggc tac 541  
Met Ile Lys His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr  
145 150 155

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Phe Leu Ile Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro  
160 165 170

ctt cca gtg ttt cac agt ctt gtg gaa ctt caa gaa aca ttt ggt tca 637  
Leu Pro Val Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Gly Ser  
175 180 185

gca ttg ctg agc agc agg tat tta tgt gtt gag tca tgg cca tct gat 685  
Ala Leu Leu Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp

190	195	200	205	
tca tac aga att gcc ttt act atc tct tta ttg cta gtt cag tat att				733
Ser Tyr Arg Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile				
210	215	220		
ctg ccc tta gtt tgt ctt act gta agt cat aca agt gtc tgc aga agt				781
Leu Pro Leu Val Cys Leu Thr Val Ser His Thr Ser Val Cys Arg Ser				
225	230	235		
ata agc tgt gga ttg tcc aac aaa gaa aac aga ctt gaa gaa aat gag				829
Ile Ser Cys Gly Leu Ser Asn Lys Glu Asn Arg Leu Glu Glu Asn Glu				
240	245	250		
atg atc aac tta act ctt cat cca tcc aaa aag agt ggg cct cag gtg				877
Met Ile Asn Leu Thr Leu His Pro Ser Lys Lys Ser Gly Pro Gln Val				
255	260	265		
aaa ctc tct ggc agc cat aaa tgg agt tat tca ttc atc aaa aaa cac				925
Lys Leu Ser Gly Ser His Lys Trp Ser Tyr Ser Phe Ile Lys Lys His				
270	275	280	285	
aga aga aga tat agc aag aag aca gca tgt gtg tta cct gct cca gaa				973
Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Glu				
290	295	300		
aga cct tct caa gag aac cac tcc aga ata ctt cca gaa aac ttt ggc				1021
Arg Pro Ser Gln Glu Asn His Ser Arg Ile Leu Pro Glu Asn Phe Gly				
305	310	315		
tct gta aga agt cag ctc tct tca tcc agt aag ttc ata cca ggg gtc				1069
Ser Val Arg Ser Gln Leu Ser Ser Ser Lys Phe Ile Pro Gly Val				
320	325	330		
ccc act tgc ttt gag ata aaa cct gaa gaa aat tca gat gtt cat gaa				1117
Pro Thr Cys Phe Glu Ile Lys Pro Glu Glu Asn Ser Asp Val His Glu				
335	340	345		
ttg aga gta aaa cgt tct gtt aca aga ata aaa aag aga tct cga agt				1165
Leu Arg Val Lys Arg Ser Val Thr Arg Ile Lys Lys Arg Ser Arg Ser				
350	355	360	365	
gtt ttc tac aga ctg acc ata ctg ata tta gta ttt gct gtt agt tgg				1213
Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp				
370	375	380		
atg cca cta cac ctt ttc cat gtg gta act gat ttt aat gac aat ctt				1261
Met Pro Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu				
385	390	395		
att tca aat agg cat ttc aag ttg gtg tat tgc att tgt cat ttg ttg				1309
Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu				
400	405	410		
ggc atg atg tcc tgt ctt aat cca att cta tat ggg ttt ctt aat				1357
Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn				
415	420	425		
aat ggg att aaa gct gat tta gtg tcc ctt ata cac tgt ctt cat atg				1405
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430

435

440

445

taa taattctcac tgttt

1423

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20 25 30

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35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met  
50 55 60

Ala Leu Met Lys Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile  
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro  
85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val  
100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser  
115 120 125

Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys  
130 135 140

His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile  
145 150 155 160

Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val  
165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu  
180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg  
195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Val Gln Tyr Ile Leu Pro Leu  
210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Arg Ser Ile Ser Cys  
225 230 235 240

Gly Leu Ser Asn Lys Glu Asn Arg Leu Glu Glu Asn Glu Met Ile Asn  
245 250 255

Leu Thr Leu His Pro Ser Lys Lys Ser Gly Pro Gln Val Lys Leu Ser  
260 265 270

Gly Ser His Lys Trp Ser Tyr Ser Phe Ile Lys Lys His Arg Arg Arg  
275 280 285

Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Glu Arg Pro Ser  
290 295 300

Gln Glu Asn His Ser Arg Ile Leu Pro Glu Asn Phe Gly Ser Val Arg  
305 310 315 320

Ser Gln Leu Ser Ser Ser Lys Phe Ile Pro Gly Val Pro Thr Cys  
325 330 335

Phe Glu Ile Lys Pro Glu Glu Asn Ser Asp Val His Glu Leu Arg Val  
340 345 350

Lys Arg Ser Val Thr Arg Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr  
355 360 365

Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro Leu  
370 375 380

His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn  
385 390 395 400

Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met Met  
405 410 415

Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile  
420 425 430

Lys Ala Asp Leu Val Ser Leu Ile His Cys Leu His Met  
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tggtctccat ctcccgaacct cgtgatccac ccacctcgac ctcccaaagt gctgggattta 180  
caggcgtgag accgcgccccg gccaatttcc tttcttagtt gcctctgccc acctttctc 240  
ttctgcttcc atattacagg ttccctcaagt tgcgaaattta ggatgttaat tatagtttt 300  
gacataacaag aaacatcaaa aagattgaat gtcttaataa gagtgaagca tgttagatcag 360  
tgactgct atg ttc atc atg aat gag aaa tgg gac aca aac tct tca gaa 410  
Met Phe Ile Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu  
1 5 10  
aac tgg cat ccc atc tgg aat gtc aat gac aca aag cat cat ctg tac 458  
Asn Trp His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr  
15 20 25 30  
tca gat att aat att acc tat gtg aac tac tat ctt cac cag cct caa 506  
Ser Asp Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln  
35 40 45  
gtg gca gca atc ttc att att tcc tac ttt ctg atc ttc ttt ttg tgc 554  
Val Ala Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys  
50 55 60  
atg atg gga aat act gtg gtt tgc ttt att gta atg agg aac aaa cat 602  
Met Met Gly Asn Thr Val Val Cys Phe Ile Val Met Arg Asn Lys His  
65 70 75  
atg cac aca gtc act aat ctc ttc atc tta aac ctg gcc ata agt gat 650  
Met His Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp  
80 85 90  
tta cta gtt ggc ata ttc tgc atg cct ata aca ctg ctg gac aat att 698  
Leu Leu Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile  
95 100 105 110  
ata gca gga tgg cca ttt gga aac acg atg tgc aag atc agt gga ttg 746  
Ile Ala Gly Trp Pro Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu  
115 120 125  
gtc cag gga ata tct gtc gca gct tca gtc ttt acg tta gtt gca att 794

Val Gln Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile			
130	135	140	
gct gta gat agg ttc cag tgt gtc tac cct ttt aaa cca aag ctc			842
Ala Val Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu			
145	150	155	
act atc aag aca gcg ttt gtc att att atg atc atc tgg gtc cta gcc			890
Thr Ile Lys Thr Ala Phe Val Ile Ile Met Ile Trp Val Leu Ala			
160	165	170	
atc acc att atg tct cca tct gca gta atg tta cat gtg caa gaa gaa			938
Ile Thr Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu			
175	180	185	190
aaa tat tac cga gtg aga ctc aac tcc cag aat aaa acc agt cca gtc			986
Lys Tyr Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val			
195	200	205	
tac tgg tgc cgg gaa gac tgg cca aat cag gaa atg agg aag atc tac			1034
Tyr Trp Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr			
210	215	220	
acc act gtg ctg ttt gcc aac atc tac ctg gct ccc ctc tcc ctc att			1082
Thr Thr Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile			
225	230	235	
gtc atc atg tat gga agg att gga att tca ctc ttc agg gct gca gtt			1130
Val Ile Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val			
240	245	250	
cct cac aca ggc agg aag aac cag gag cag tgg cac gtg gtg tcc agg			1178
Pro His Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg			
255	260	265	270
aag aag cag aag atc att aag atg ctc ctg att gtg gcc ctg ctt ttt			1226
Lys Lys Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe			
275	280	285	
att ctc tca tgg ctg ccc ctg tgg act cta atg atg ctc tca gac tac			1274
Ile Leu Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr			
290	295	300	
gct gac ctt tct cca aat gaa ctg cag atc atc aac atc tac atc tac			1322
Ala Asp Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr			
305	310	315	
cct ttt gca cac tgg ctg gca ttc ggc aac agc agt gtc aat ccc atc			1370
Pro Phe Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile			
320	325	330	
att tat ggt ttc ttc aac gag aat ttc cgc cgt ggt ttc caa gaa gct			1418
Ile Tyr Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala			
335	340	345	350
ttc cag ctc cag ctc tgc caa aaa aga gca aag cct atg gaa gct tat			1466
Phe Gln Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr			
355	360	365	
acc cta aaa gct aaa agc cat gtg ctc ata aac aca tct aat cag ctt			1514

Thr	Leu	Lys	Ala	Lys	Ser	His	Val	Leu	Ile	Asn	Thr	Ser	Asn	Gln	Leu	
370								375						380		
gtc	cag	gaa	tct	aca	ttt	caa	aac	cct	cat	ggg	gaa	acc	ttg	ctt	tat	1562
Val	Gln	Glu	Ser	Thr	Phe	Gln	Asn	Pro	His	Gly	Glu	Thr	Leu	Leu	Tyr	
385						390							395			
agg	aaa	agt	gct	gaa	aac	ccc	aac	agg	aat	tag	tgatggaaga	attaaaagaa				1615
Arg	Lys	Ser	Ala	Glu	Asn	Pro	Asn	Arg	Asn							
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ttatatattt	aaatccattt	ctttttgtgg	ctttgcactt	caaatttttc	aaagaatgtt											1735
ctaaataaaa	catttactga	aagcccttc	tggcaaaaaa	attaaaaata	aacaaaaatg											1795
gtcataagat	cataaacaat	cttatgttgt	ataaaaatac	gtagagtgac	tttagacatgt											1855
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His	Pro	Ile	Trp	Asn	Val	Asn	Asp	Thr	Lys	His	His	Leu	Tyr	Ser	Asp	
					20				25					30		
Ile	Asn	Ile	Thr	Tyr	Val	Asn	Tyr	Tyr	Leu	His	Gln	Pro	Gln	Val	Ala	
					35			40						45		
Ala	Ile	Phe	Ile	Ile	Ser	Tyr	Phe	Leu	Ile	Phe	Phe	Leu	Cys	Met	Met	
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Gly	Asn	Thr	Val	Val	Cys	Phe	Ile	Val	Met	Arg	Asn	Lys	His	Met	His	
					65			70						75		80
Thr	Val	Thr	Asn	Leu	Phe	Ile	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Leu	
					85				90					95		
Val	Gly	Ile	Phe	Cys	Met	Pro	Ile	Thr	Leu	Leu	Asp	Asn	Ile	Ile	Ala	
					100				105					110		
Gly	Trp	Pro	Phe	Gly	Asn	Thr	Met	Cys	Lys	Ile	Ser	Gly	Leu	Val	Gln	
					115				120					125		

Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val  
130 135 140

Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile  
145 150 155 160

Lys Thr Ala Phe Val Ile Ile Met Ile Trp Val Leu Ala Ile Thr  
165 170 175

Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr  
180 185 190

Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp  
195 200 205

Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr  
210 215 220

Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile  
225 230 235 240

Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His  
245 250 255

Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys  
260 265 270

Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu  
275 280 285

Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp  
290 295 300

Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe  
305 310 315 320

Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr  
325 330 335

Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln  
340 345 350

Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu  
355 360 365

Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln  
370 375 380

Glu Ser Thr Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys  
385 390 395 400

Ser Ala Glu Asn Pro Asn Arg Asn  
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caaaacataa aaaa atg aac tca act ctg ttc tcc aag gtt gaa aat cac 170  
Met Asn Ser Thr Leu Phe Ser Lys Val Glu Asn His  
1 5 10  
tca att cac tat aat gcc tca gag aat tct cca ctt ctg gct ttt gaa 218  
Ser Ile His Tyr Asn Ala Ser Glu Asn Ser Pro Leu Leu Ala Phe Glu  
15 20 25  
aat gat gac tgc cac ctg ccc ttg gct gtg ata ttc acc ttg gct ctc 266  
Asn Asp Asp Cys His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu  
30 35 40  
gct tat ggg gcg gtg att att ctt ggc gtc tct gga aac ctg gca ttg 314  
Ala Tyr Gly Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu  
45 50 55 60  
atc ata atc att ctg aaa cag aag gag atg aga aat gtc acc aac att 362  
Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile  
65 70 75  
ctg atc gtg aac ctc tcc ttc tca gac ttg ctc gtt gcg gtc atg tgt 410  
Leu Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys  
80 85 90  
ctc ccg ttc act ttt gta tat aca ctg atg gac cac tgg gtc ttc ggg 458  
Leu Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly  
95 100 105  
gag acc atg tgc aaa ctg aat ccc ttt gta cag tgt gtc tcc atc aca 506  
Glu Thr Met Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr  
110 115 120

gta tcc att ttc tcg ctg gtt ctc atc gct gtg gaa cgg cat cag cta Val Ser Ile Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu 125 130 135 140	554
atc atc aac cca aga ggg tgg aga cca aac aat aga cat gct tac ata Ile Ile Asn Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile 145 150 155	602
ggc att act gtc att tgg gtc ctt gca gtg gct tct tct ctg ccc ttt Gly Ile Thr Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe 160 165 170	650
gtg atc tat caa att ctg acc gac gag ccc ttc caa aat gtg tca ctt Val Ile Tyr Gln Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu 175 180 185	698
gcg gcg ttc aag gac aag tat gtg tgc ttt gac aaa ttc cca tct gac Ala Ala Phe Lys Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp 190 195 200	746
tct cac agg ctg tct tac acg act ctc ctc ctg gtg ctg cag tat ttc Ser His Arg Leu Ser Tyr Thr Leu Leu Leu Val Leu Gln Tyr Phe 205 210 215 220	794
ggc cca ctc tgc ttt ata ttc ata tgc tac ttc aag ata tac att cgc Gly Pro Leu Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg 225 230 235	842
ttg aaa agg aga aac aac atg atg gac aag atc cgg gac agt aag tac Leu Lys Arg Arg Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr 240 245 250	890
agg tcc agt gag acc aag cga atc aac atc atg ctg ctc tcc att gtg Arg Ser Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val 255 260 265	938
gtc gcc ttc gcc gtc tgg ctg ccc ctt acc atc ttc aac act gtg Val Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val 270 275 280	986
ttc gac tgg aac cac cag atc att gcc acc tgc aac cac aat ctg ctg Phe Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu 285 290 295 300	1034
ttt ctg ctc tgt cac ctc acc gcc atg atc tcc acc tgc gtc aac ccc Phe Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro 305 310 315	1082
atc ttt tat gga ttc ctg aac aaa aat ttc cag aga gac ttg cag ttc Ile Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe 320 325 330	1130
ttc ttc aac ttt tgt gac ttc cgg tct cga gac gat gac tac gag acc Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr 335 340 345	1178
ata gcc atg tct acc atg cat acg gat gtg tcc aag acg tct ctg aag Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys 350 355 360	1226

cag gct agc cca gtc gca ttt aaa aaa atc agt atg aat gac aat gaa 1274  
Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu  
365 370 375 380

aaa gtc tga agctgctcag agcatatggt cccaggccat atctgtggaa 1323  
Lys Val

aaacaagcac agcctgccgc atgctttctt tacctatgct ctgggggaac ggaatgaggc 1383  
gcgcggaa agcccaggac atctgtgtta aatttgactg cttttgatgg ttgccctgat 1443  
tacttagaaa tctagattac tttgtaatct atctctggca acagtttga ctagatgtcc 1503  
tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgta tgtgtgtcg 1563  
cgcgcgcg cgcgcacgtg caaaagagaa agagagagag agaaggagag agacagacag 1623  
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caaagagtt tacattgtgt ttgttggagt gaatttctct gaagtaatgt catgagctca 1743  
tttcaaaagc agtcaccacc tgatattctc gagaggctga atttcaaga tcagatgaga 1803  
tttccgagac cccggactac ctgcgttccc tgctaggcat catcttagtc tgtcacaagg 1863  
gtgacagtat acaaagtcac cttttgaat gtgcctgagt caaaagagtg tctgaagtca 1923  
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<210> 12  
<211> 382  
<212> PRT  
<213> mouse neuropeptide Y1 receptor

<400> 12

Met Asn Ser Thr Leu Phe Ser Lys Val Glu Asn His Ser Ile His Tyr  
1 5 10 15

Asn Ala Ser Glu Asn Ser Pro Leu Leu Ala Phe Glu Asn Asp Asp Cys  
20 25 30

His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu Ala Tyr Gly Ala  
35 40 45

Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile  
50 55 60

Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn  
65 70 75 80

Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr  
85 90 95

Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys  
100 105 110

Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe  
115 120 125

Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro  
130 135 140

Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val  
145 150 155 160

Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln  
165 170 175

Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys  
180 185 190

Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu  
195 200 205

Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys  
210 215 220

Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg  
225 230 235 240

Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu  
245 250 255

Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe Ala  
260 265 270

Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp Asn  
275 280 285

His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu Cys  
290 295 300

His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly  
305 310 315 320

Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Asn Phe  
325 330 335

Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser  
340 345 350

Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro  
355 360 365

Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Val  
370 375 380

<210> 13  
<211> 2650  
<212> DNA  
<213> mouse neuropeptide Y2 receptor

<220>  
<221> CDS  
<222> (781)..(1938)

<400> 13  
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cattcttagtt ggtgacttcc agaccagtga gaaggcctgt ctcaaaaaac aatgtggatg 120  
gcacctgagg aatgataacct gagggttgct tttgactata gacacagatg ttcacactga 180  
accacccaca ccccccccca cacacacacc agaggggggg ggggcttatg tgcacaagaa 240  
gtgaaaagaaa aaaggcgtgt gtgagaatcc agctgttttgc ctttattta atctccaaa 300  
gatcaggtgc tcagcacatg cagatgtttg cccctttgtt atattttagg ctgctgtata 360  
cttacacatt tcaaacaatt aagtgggtga cactttccct taagttaatg tggtgacttc 420  
atagcaatta taaaattgat aaactttattt gcattcattt tgcattaaaa tggaatttat 480  
ttgatctcac tcattgtgga gctgattctc tctctaacag gaaagtgtag ttttgtcatg 540  
atcatagata ttttgaattt ctaggttcat ccattccctag ttgttaatcg acttatgtaa 600  
aggatttgct tcatcaagct tttgcaagat ctacagtgtg atgaatcaga acacagctat 660  
ccagagagct cactctaaac taaatcaatc cctttagaat gtttctctgt ttcactaact 720  
tttttttaat gtcattttta ttatagattt ttgtgttatt tacaggccaa gtgagagtga 780  
atg gtt ctg aag atg ggc ccg gta ggt gca gag gca gat gag aat caa 828  
Met Val Leu Lys Met Gly Pro Val Gly Ala Glu Ala Asp Glu Asn Gln  
1 5 10 15  
act gta gaa gtg aaa gtg gag ccc tat ggg cca ggg cac act act cct 876  
Thr Val Glu Val Lys Val Glu Pro Tyr Gly Pro Gly His Thr Thr Pro  
20 25 30  
aga ggt gag ttg ccc cct gat ccg gag ccg gag ctc ata gac agc acc 924

Arg	Gly	Glu	Leu	Pro	Pro	Asp	Pro	Glu	Pro	Glu	Leu	Ile	Asp	Ser	Thr		
35						40						45					
aaa	ctg	gtc	gag	gtg	cag	gtg	atc	ctc	ata	ttg	gcc	tac	tgc	tcc	atc		972
Lys	Leu	Val	Glu	Val	Gln	Val	Ile	Leu	Ile	Leu	Ala	Tyr	Cys	Ser	Ile		
50						55					60						
atc	ttg	cta	ggg	gta	gtt	ggc	aac	tcc	ctg	gta	atc	cat	gtg	gta	atc		1020
Ile	Leu	Leu	Gly	Val	Val	Gly	Asn	Ser	Leu	Val	Ile	His	Val	Val	Ile		
65						70				75			80				
aaa	ttc	aag	agc	atg	cgc	aca	gta	acc	aac	ttt	ttt	att	gcc	aac	ctg		1068
Lys	Phe	Lys	Ser	Met	Arg	Thr	Val	Thr	Asn	Phe	Phe	Ile	Ala	Asn	Leu		
85						90						95					
gct	gtg	gcf	gat	ctt	ttg	gtg	aac	acc	ctg	tgc	ctg	cca	ttc	act	ctt		1116
Ala	Val	Ala	Asp	Leu	Leu	Val	Asn	Thr	Leu	Cys	Leu	Pro	Phe	Thr	Leu		
100						105						110					
acc	tat	acc	ttg	atg	gga	gag	tgg	aaa	atg	ggt	ccg	gtc	ttg	tgc	cat		1164
Thr	Tyr	Thr	Leu	Met	Gly	Glu	Trp	Lys	Met	Gly	Pro	Val	Leu	Cys	His		
115						120					125						
ttg	gtg	ccc	tat	gcc	cag	ggt	ctg	gcf	gta	caa	gtg	tcc	aca	ata	act		1212
Leu	Val	Pro	Tyr	Ala	Gln	Gly	Leu	Ala	Val	Gln	Val	Ser	Thr	Ile	Thr		
130						135					140						
ttg	aca	gtc	att	gct	ctg	gac	cgc	cat	cgt	tgc	att	gtc	tac	cac	ctg		1260
Leu	Thr	Val	Ile	Ala	Leu	Asp	Arg	Cys	Ile	Val	Tyr	His	Leu				
145						150				155		160					
gag	agc	aag	atc	tcc	aag	cga	atc	agc	ttc	ctg	atc	att	ggc	ctg	gcc		1308
Glu	Ser	Lys	Ile	Ser	Lys	Arg	Ile	Ser	Phe	Leu	Ile	Ile	Gly	Leu	Ala		
165						170					175						
tgg	ggc	atc	agc	gct	ctg	gca	agt	cca	ctg	gcc	atc	ttc	cgg	gaa			1356
Trp	Gly	Ile	Ser	Ala	Leu	Leu	Ala	Ser	Pro	Leu	Ala	Ile	Phe	Arg	Glu		
180						185					190						
tac	tcc	ctg	att	gag	atc	att	cct	gac	ttt	gag	att	gtg	gcc	tgt	acc		1404
Tyr	Ser	Leu	Ile	Glu	Ile	Ile	Pro	Asp	Phe	Glu	Ile	Val	Ala	Cys	Thr		
195						200					205						
gag	aag	tgg	cct	ggg	gaa	gag	aag	agt	gtg	tat	ggt	aca	gtc	tac	agc		1452
Glu	Lys	Trp	Pro	Gly	Glu	Glu	Lys	Ser	Val	Tyr	Gly	Thr	Val	Tyr	Ser		
210						215					220						
ctt	tcc	acc	ctg	ctc	atc	ctg	tac	gtt	ttg	cct	ctg	ggc	atc	ata	tct		1500
Leu	Ser	Thr	Leu	Leu	Ile	Leu	Tyr	Val	Leu	Pro	Leu	Gly	Ile	Ile	Ser		
225						230				235		240					
ttc	tcc	tac	acc	cgt	atc	tgg	agt	aag	ctg	agg	aac	cac	gtc	agt	cct		1548
Phe	Ser	Tyr	Thr	Arg	Ile	Trp	Ser	Lys	Leu	Arg	Asn	His	Val	Ser	Pro		
245						250				255							
gga	gct	gca	agt	gac	cat	tac	cat	cag	cga	agg	cac	aaa	atg	acc	aaa		1596
Gly	Ala	Ala	Ser	Asp	His	Tyr	His	Gln	Arg	Arg	His	Lys	Met	Thr	Lys		
260						265					270						
atg	ctg	gtc	tgc	gtg	gta	gtg	gtg	ttt	gca	gtc	agc	tgg	cta	ccc	ctc		1644

<210> 14  
<211> 385  
<212> PRT  
<213> mouse neuropeptide Y2 receptor

<400> 14

Met Val Leu Lys Met Gly Pro Val Gly Ala Glu Ala Asp Glu Asn Gln  
1 5 10 15

Thr Val Glu Val Lys Val Glu Pro Tyr Gly Pro Gly His Thr Thr Pro  
20 25 30

Arg Gly Glu Leu Pro Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr  
35 40 45

Lys Leu Val Glu Val Gln Val Ile Leu Ile Leu Ala Tyr Cys Ser Ile  
50 55 60

Ile Leu Leu Gly Val Val Gly Asn Ser Leu Val Ile His Val Val Ile  
65 70 75 80

Lys Phe Lys Ser Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu  
85 90 95

Ala Val Ala Asp Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu  
100 105 110

Thr Tyr Thr Leu Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His  
115 120 125

Leu Val Pro Tyr Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr  
130 135 140

Leu Thr Val Ile Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu  
145 150 155 160

Glu Ser Lys Ile Ser Lys Arg Ile Ser Phe Leu Ile Ile Gly Leu Ala  
165 170 175

Trp Gly Ile Ser Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu  
180 185 190

Tyr Ser Leu Ile Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr  
195 200 205

Glu Lys Trp Pro Gly Glu Glu Lys Ser Val Tyr Gly Thr Val Tyr Ser  
210 215 220

Leu Ser Thr Leu Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser

225	230	235	240
Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Arg Asn His Val Ser Pro			
245		250	255
Gly Ala Ala Ser Asp His Tyr His Gln Arg Arg His Lys Met Thr Lys			
260		265	270
Met Leu Val Cys Val Val Val Phe Ala Val Ser Trp Leu Pro Leu			
275		280	285
His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser His Val Leu Asp Leu			
290		295	300
Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys			
305		310	315
Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr			
325		330	335
Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala			
340		345	350
Ile His Ser Glu Val Ser Met Thr Phe Lys Ala Lys Lys Asn Leu Glu			
355		360	365
Val Lys Lys Asn Asn Gly Pro Thr Asp Ser Phe Ser Glu Ala Thr Asn			
370		375	380
Val			
385			
<210> 15			
<211> 1709			
<212> DNA			
<213> mouse neuropeptide Y4 receptor			
<220>			
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<222> (204)..(1331)			
<400> 15			
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ccaagaacct tttcccttgc ccttatcggtt acctgggtcc attgttagatg catggtcctt			120
gagttccatt tgtttgaaaa gcaggctgca tctctgaagt agggccctta ctcctggagt			180

tcccgatct tctcacacct acc atg aat acc tct cat ttc ttg gcc cct ctc		233
Met Asn Thr Ser His Phe Leu Ala Pro Leu		
1 5 10		
ttc cca gga tcc cta cag ggt aag aat ggg acc aat cca ttg gat tcc		281
Phe Pro Gly Ser Leu Gln Gly Lys Asn Gly Thr Asn Pro Leu Asp Ser		
15 20 25		
ccc tat aat ttc tct gat ggc tgc cag gat tcg gca gaa ctg ttg gcc		329
Pro Tyr Asn Phe Ser Asp Gly Cys Gln Asp Ser Ala Glu Leu Leu Ala		
30 35 40		
ttc atc atc acc acc tac agc att gag acc atc tta ggg gtc ctg gga		377
Phe Ile Ile Thr Thr Tyr Ser Ile Glu Thr Ile Leu Gly Val Leu Gly		
45 50 55		
aac ctc tgc ttg ata ttt gtg acc aca aga caa aag gaa aag tcc aat		425
Asn Leu Cys Leu Ile Phe Val Thr Thr Arg Gln Lys Glu Lys Ser Asn		
60 65 70		
gtg acc aac cta ctc att gcc aac ctg gcc ttc tct gac ttc ctc atg		473
Val Thr Asn Leu Leu Ile Ala Asn Leu Ala Phe Ser Asp Phe Leu Met		
75 80 85 90		
tgc ctc atc tgc caa cca ctc aca gtc acc tac acc atc atg gat tac		521
Cys Leu Ile Cys Gln Pro Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr		
95 100 105		
tgg atc ttt ggt gaa gtc ctt tgc aag atg tta act ttc atc cag tgt		569
Trp Ile Phe Gly Glu Val Leu Cys Lys Met Leu Thr Phe Ile Gln Cys		
110 115 120		
atg tca gtg aca gtc tcc atc ctc tca ctg gtc ctt gtg gcc ctg gag		617
Met Ser Val Thr Val Ser Ile Leu Ser Leu Val Leu Val Ala Leu Glu		
125 130 135		
aga cac cag ctc att atc aat cca aca ggc tgg aaa ccc agt att ttc		665
Arg His Gln Leu Ile Ile Asn Pro Thr Gly Trp Lys Pro Ser Ile Phe		
140 145 150		
cag gcc tac ctg ggg att gtg gtc atc tgg ttc atc tct tgt ttc ctt		713
Gln Ala Tyr Leu Gly Ile Val Val Ile Trp Phe Ile Ser Cys Phe Leu		
155 160 165 170		
tcc ttg ccg ttc ctg gcc aac agc acc ctg aat gac ctc ttc cac tac		761
Ser Leu Pro Phe Leu Ala Asn Ser Thr Leu Asn Asp Leu Phe His Tyr		
175 180 185		
aac cac tct aag gtt gag ttt ctg gaa gac aag gtc gtc tgc ttt		809
Asn His Ser Lys Val Val Glu Phe Leu Glu Asp Lys Val Val Cys Phe		
190 195 200		
gtg tcc tgg tct tca gat cac cac cgt ctc atc tat acc acc ttt ctg		857
Val Ser Trp Ser Ser Asp His His Arg Leu Ile Tyr Thr Thr Phe Leu		
205 210 215		
ctg ctc ttt cag tac tgc atc cct cta gcc ttc atc ctg gtc tgc tac		905
Leu Leu Phe Gln Tyr Cys Ile Pro Leu Ala Phe Ile Leu Val Cys Tyr		
220 225 230		

ata cgc atc tac cag cgc ctg cag agg cat gtc ttc cat gcg Ile Arg Ile Tyr Gln Arg Leu Gln Arg Gln Lys His Val Phe His Ala 235	240	245	250	953
cac gct tgc agc tca cga gcg ggg cag atg aag cgg atc aac agc atg His Ala Cys Ser Ser Arg Ala Gly Gln Met Lys Arg Ile Asn Ser Met 255	260	265		1001
ctc atg aca atg gtg act gcc ttt gca gtt ctc tgg cta ccc ctg cat Leu Met Thr Met Val Thr Ala Phe Ala Val Leu Trp Leu Pro Leu His 270	275	280		1049
gtg ttc aac act ctg gag gac tgg tac cag gaa gcc atc cct gct tgc Val Phe Asn Thr Leu Glu Asp Trp Tyr Gln Glu Ala Ile Pro Ala Cys 285	290	295		1097
cat ggc aac ctc atc ttc ttg atg tgc cac ctg ttg gcc atg gct tcc His Gly Asn Leu Ile Phe Leu Met Cys His Leu Leu Ala Met Ala Ser 300	305	310		1145
acc tgt gtc aac cct ttc atc tat ggc ttt ctc aac atc aac ttc aag Thr Cys Val Asn Pro Phe Ile Tyr Gly Phe Leu Asn Ile Asn Phe Lys 315	320	325	330	1193
aag gat atc aag gct ctg gtg ctg acc tgc cat tgc agg tca cct caa Lys Asp Ile Lys Ala Leu Val Leu Thr Cys His Cys Arg Ser Pro Gln 335	340	345		1241
ggg gag tct gag cat ctg ccc ctg tcc act gtt cac acg gac ctc tcc Gly Glu Ser Glu His Leu Pro Leu Ser Thr Val His Thr Asp Leu Ser 350	355	360		1289
aag gga tcg atg agg atg ggt agc aag tct aac ttc ata tag Lys Gly Ser Met Arg Met Gly Ser Lys Ser Asn Phe Ile 365	370	375		1331
tttgtctgg gctttccct accattttt ttgacacatc ctttactta gttttagaaaa cacattgcag gctgtatag catcctgtca ttctggctt ttggggccca gatagggtgg caagagactt gaagcttggc attcagatgg tttagccctt tgcttctgag agatctctga gtcaggattc tgcatcactac agagggact ttgtggcttg agctgcaagg gtatttagagt cagaagtggc tgactctcac agccactcag tacagatgcc tggccaaaa gccttcatct atgtcctgac cattcagcta acctgcctt ggttatgtgc ttatgttctt ccaagggatg ttgggtgttt cagttatgg				1391 1451 1511 1571 1631 1691 1709

<210> 16  
<211> 375  
<212> PRT  
<213> mouse neuropeptide Y4 receptor

<400> 16

Met	Asn	Thr	Ser	His	Phe	Leu	Ala	Pro	Leu	Phe	Pro	Gly	Ser	Leu	Gln
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Gly Lys Asn Gly Thr Asn Pro Leu Asp Ser Pro Tyr Asn Phe Ser Asp  
20 25 30

Gly Cys Gln Asp Ser Ala Glu Leu Leu Ala Phe Ile Ile Thr Thr Tyr  
35 40 45

Ser Ile Glu Thr Ile Leu Gly Val Leu Gly Asn Leu Cys Leu Ile Phe  
50 55 60

Val Thr Thr Arg Gln Lys Glu Lys Ser Asn Val Thr Asn Leu Leu Ile  
65 70 75 80

Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Ile Cys Gln Pro  
85 90 95

Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Val  
100 105 110

Leu Cys Lys Met Leu Thr Phe Ile Gln Cys Met Ser Val Thr Val Ser  
115 120 125

Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile  
130 135 140

Asn Pro Thr Gly Trp Lys Pro Ser Ile Phe Gln Ala Tyr Leu Gly Ile  
145 150 155 160

Val Val Ile Trp Phe Ile Ser Cys Phe Leu Ser Leu Pro Phe Leu Ala  
165 170 175

Asn Ser Thr Leu Asn Asp Leu Phe His Tyr Asn His Ser Lys Val Val  
180 185 190

Glu Phe Leu Glu Asp Lys Val Val Cys Phe Val Ser Trp Ser Ser Asp  
195 200 205

His His Arg Leu Ile Tyr Thr Phe Leu Leu Leu Phe Gln Tyr Cys  
210 215 220

Ile Pro Leu Ala Phe Ile Leu Val Cys Tyr Ile Arg Ile Tyr Gln Arg  
225 230 235 240

Leu Gln Arg Gln Lys His Val Phe His Ala His Ala Cys Ser Ser Arg  
245 250 255

Ala Gly Gln Met Lys Arg Ile Asn Ser Met Leu Met Thr Met Val Thr  
260 265 270

Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Thr Leu Glu  
275 280 285

Asp Trp Tyr Gln Glu Ala Ile Pro Ala Cys His Gly Asn Leu Ile Phe  
290 295 300

Leu Met Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe  
305 310 315 320

Ile Tyr Gly Phe Leu Asn Ile Asn Phe Lys Lys Asp Ile Lys Ala Leu  
325 330 335

Val Leu Thr Cys His Cys Arg Ser Pro Gln Gly Glu Ser Glu His Leu  
340 345 350

Pro Leu Ser Thr Val His Thr Asp Leu Ser Lys Gly Ser Met Arg Met  
355 360 365

Gly Ser Lys Ser Asn Phe Ile  
370 375

<210> 17  
<211> 1868  
<212> DNA  
<213> mouse neuropeptide Y5 receptor

<220>  
<221> CDS  
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Met Glu Val Lys Leu  
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gaa gag cat ttt aac aag aca ttt gtc acg gag aac aat act gct gcc 162  
Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala  
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agt cag aac acg gcc tcc cct gcc tgg gag gac tac aga ggc aca gag 210  
Ser Gln Asn Thr Ala Ser Pro Ala Trp Glu Asp Tyr Arg Gly Thr Glu  
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aac aat act tct gct gct cgg aac act gcc ttt cca gtc tgg gag gac 258

Asn Asn Thr Ser Ala Ala Arg Asn Thr Ala Phe Pro Val Trp Glu Asp			
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tat aga ggc agc gta gac gac tta caa tac ttc ctg att ggg ctc tat			306
Tyr Arg Gly Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr			
55	60	65	
aca ttt gta agt ctt ctt ggt ttt atg gga aat cta ctt atc tta atg			354
Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met			
70	75	80	85
gct gtt atg aaa aag cgc aat cag aag act aca gtg aac ttt ctc ata			402
Ala Val Met Lys Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile			
90	95	100	
ggc aac ctg gcc ttc tcc gac att ttg gtt gtc ctg ttt tgc tcc cct			450
Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro			
105	110	115	
ttc acc ctg acc tct gtc ttg ttg gat cag tgg atg ttc ggc aaa gcc			498
Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Ala			
120	125	130	
atg tgc cat atc atg cca ttc ctt cag tgt gta tca gtt ctg gtt tca			546
Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser			
135	140	145	
act ctg att tta ata tcg att gcc att gtc agg tat cat atg ata aag			594
Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys			
150	155	160	165
cac cct ata tct aac aat tta aca gca aac cat ggc tac ttc ctg ata			642
His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile			
170	175	180	
gct act gtc tgg aca ctg ggc ttt gcc atc tgt tct ccc ctc cca gtg			690
Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val			
185	190	195	
ttt cac agc ctt gtg gaa ctt aag gaa acc ttt ggc tca gca ttg cta			738
Phe His Ser Leu Val Glu Leu Lys Glu Thr Phe Gly Ser Ala Leu Leu			
200	205	210	
agc agc aag tat ttg tgt gtt gag tca tgg ccc tct gat tca tac aga			786
Ser Ser Lys Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg			
215	220	225	
att gct ttc aca atc tct tta ttg tta gtt cag tat atc ctg cct cta			834
Ile Ala Phe Thr Ile Ser Leu Leu Val Gln Tyr Ile Leu Pro Leu			
230	235	240	245
gta tgt tta aca gta agt cat act agt gtc tgc agg agt ata agc tgt			882
Val Cys Leu Thr Val Ser His Thr Ser Val Cys Arg Ser Ile Ser Cys			
250	255	260	
gga ttg tcc cac aaa gaa aac aga ctc gaa gaa aat gag atg atc aac			930
Gly Leu Ser His Lys Glu Asn Arg Leu Glu Glu Asn Glu Met Ile Asn			
265	270	275	
tta act cta cat cca tcc aaa aag agt cgg gac cag gca aaa ccc ccc			978

Leu Thr Leu His Pro Ser Lys Lys Ser Arg Asp Gln Ala Lys Pro Pro			
280	285	290	
agc act caa aag tgg agc tac tca ttc atc aga aag cac cga aga agg			1026
Ser Thr Gln Lys Trp Ser Tyr Ser Phe Ile Arg Lys His Arg Arg Arg			
295	300	305	
tac agc aag aag acg gca tgc gtg tta ccc gcc cca gca gga cct tcc			1074
Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Ala Gly Pro Ser			
310	315	320	325
cag gag aag cac cta acc gtt cca gaa aac cca ggc tcg gtc cgt agc			1122
Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro Gly Ser Val Arg Ser			
330	335	340	
cag ctg tca cca tcc agt aag gtt att cca ggg gtc ccg atc tgc ttt			1170
Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly Val Pro Ile Cys Phe			
345	350	355	
gag gtg aaa cct gaa gaa agc tca gat gct cag gag atg aga gtc aag			1218
Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln Glu Met Arg Val Lys			
360	365	370	
cgt tcc ctc acg aga ata aag aag aga tct cgc agt gtt ttc tac aga			1266
Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg			
375	380	385	
ctg act ata ttg ata tta gtg ttc gct gtt agc tgg atg cca ctc cac			1314
Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro Leu His			
390	395	400	405
gtc ttc cac gtg gtg acc gat ttc aat gat aac ctg att tcc aat agg			1362
Val Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg			
410	415	420	
cat ttc aag ctg gtg tac tgc atc tgt cac ttg tta ggc atg atg tcc			1410
His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser			
425	430	435	
tgt tgt ctt aat ccg atc tta tat gga ttc ctt aat aat ggt atc aaa			1458
Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys			
440	445	450	
gca gac ttg aga gcc ctt atc cac tgc cta cac atg tca tga			1500
Ala Asp Leu Arg Ala Leu Ile His Cys Leu His Met Ser			
455	460	465	
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agatcattta tggtataatg tggttaattc cgtcaattgt gcagagtcaa tgtcgatcta			1680
aggaaatttc tgtcttgaaa tagttacatt accgtccatt tcatgtcatt ggtaataagt			1740
tgagtgtctt cggtttcgag taaaagttat agctatccaa attgttattt tgtacaaaaa			1800
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Tyr Arg Gly Thr Glu Asn Asn Thr Ser Ala Ala Arg Asn Thr Ala Phe  
35 40 45

Pro Val Trp Glu Asp Tyr Arg Gly Ser Val Asp Asp Leu Gln Tyr Phe  
50 55 60

Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn  
65 70 75 80

Leu Leu Ile Leu Met Ala Val Met Lys Lys Arg Asn Gln Lys Thr Thr  
85 90 95

Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val  
100 105 110

Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp  
115 120 125

Met Phe Gly Lys Ala Met Cys His Ile Met Pro Phe Leu Gln Cys Val  
130 135 140

Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg  
145 150 155 160

Tyr His Met Ile Lys His Pro Ile Ser Asn Asn Leu Thr Ala Asn His  
165 170 175

Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys  
180 185 190

Ser Pro Leu Pro Val Phe His Ser Leu Val Glu Leu Lys Glu Thr Phe  
195 200 205

Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu Cys Val Glu Ser Trp Pro  
210 215 220

Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln  
225 230 235 240

Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser His Thr Ser Val Cys  
245 250 255

Arg Ser Ile Ser Cys Gly Leu Ser His Lys Glu Asn Arg Leu Glu Glu  
260 265 270

Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser Lys Lys Ser Arg Asp  
275 280 285

Gln Ala Lys Pro Pro Ser Thr Gln Lys Trp Ser Tyr Ser Phe Ile Arg  
290 295 300

Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala  
305 310 315 320

Pro Ala Gly Pro Ser Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro  
325 330 335

Gly Ser Val Arg Ser Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly  
340 345 350

Val Pro Ile Cys Phe Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln  
355 360 365

Glu Met Arg Val Lys Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg  
370 375 380

Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser  
385 390 395 400

Trp Met Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn  
405 410 415

Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu  
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Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu  
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Met Ser  
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 cttcgttac tgcttctgaa gcctatactg atagaattaa taaaatactg agagagagag 180  
 agagggacag agagagagag ggggagagag agagagagag agagagagag agagagagag 240  
 agagagagag agaagagaag aaaacaaggt saagccatct gcttaactta tgtccacatt 300  
 ctctcaagag cattgtccta tttgtagaat tatctatatt gttaagaatc atctccattg 360  
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 aagtccatgg ttctattccc aaggctacat aaaaccttgt gttgtatga atgcctgtaa 480  
 tcccagtacg cagcaaggag agacaaggag gatcagaagc ttaaggacat cattttgtac 540  
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 aaacaaaaaca aaaccttcta ctaatattct ggattctgtt tgatTTTtag gatctcaaga 660  
 gcatgctgac gtcatttatg tgTTTccatc agatacagac agagatcata aacatttaac 720  
 tcattgatta tatgttgaga gttgtccctc aagaaccaat ggccaaacat ccactgagga 780  
 tacacggaag ctttagaaaat ctctaattaa aatcctgaca ta atg gaa gtg ctc 834  
 Met Glu Val Leu  
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aca aac cag cca aca cct aat aaa acc agt ggc aag agc aac aac tcg 882  
 Thr Asn Gln Pro Thr Pro Asn Lys Thr Ser Gly Lys Ser Asn Asn Ser  
 5 10 15 20

gca ttt ttc tac ttt gaa tcc tgc caa ccc cct ttt cta gcc ata ctc 930  
 Ala Phe Phe Tyr Phe Glu Ser Cys Gln Pro Pro Phe Leu Ala Ile Leu  
 25 30 35

ttg cta ctc ata gca tat act gtg atc cta atc atg ggc att ttt gga 978  
 Leu Leu Leu Ile Ala Tyr Thr Val Ile Leu Ile Met Gly Ile Phe Gly

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aac ctc tct ctt atc atc atc ttt aag aaa cag aga gaa gct caa Asn Leu Ser Leu Ile Ile Ile Phe Lys Lys Gln Arg Glu Ala Gln 55	60	65	1026
aat gtt acc aac ata ctg att gcc aac ctg tcc ctc tct gac atc ttg Asn Val Thr Asn Ile Leu Ile Ala Asn Leu Ser Leu Ser Asp Ile Leu 70	75	80	1074
gtg tgt gtc atg tgc atc cct ttt acg gtc atc tac act ctg atg gac Val Cys Val Met Cys Ile Pro Phe Thr Val Ile Tyr Thr Leu Met Asp 85	90	95	1122
cac tgg gta ttt ggg aac act atg tgt aaa ctc act tcc tac gtg caa His Trp Val Phe Gly Asn Thr Met Cys Lys Leu Thr Ser Tyr Val Gln 105	110	115	1170
agt gtc tca gtt tct gtg tcc ata ttc tcc ctt gtg ttg att gct att Ser Val Ser Val Ser Ile Phe Ser Leu Val Leu Ile Ala Ile 120	125	130	1218
gaa cga tat cag ctg att gtg aac ccc cgt ggc tgg aaa ccc aga gta Glu Arg Tyr Gln Leu Ile Val Asn Pro Arg Gly Trp Lys Pro Arg Val 135	140	145	1266
gct cat gcc tat tgg ggg atc atc ttg att tgg ctc att tct ctg aca Ala His Ala Tyr Trp Gly Ile Ile Leu Ile Trp Leu Ile Ser Leu Thr 150	155	160	1314
ttg tct att ccc tta ttc ctg tcc tac cac ctc acc aat gag ccc ttt Leu Ser Ile Pro Leu Phe Leu Ser Tyr His Leu Thr Asn Glu Pro Phe 165	170	175	1362
cat aat ctc tct ctc cct act gac atc tac acc cac cag gta gct tgt His Asn Leu Ser Leu Pro Thr Asp Ile Tyr Thr His Gln Val Ala Cys 185	190	195	1410
gtg gag att tgg cct tct aaa ctg aac caa ctc ctc ttt tct aca tca Val Glu Ile Trp Pro Ser Lys Leu Asn Gln Leu Leu Phe Ser Thr Ser 200	205	210	1458
tta ttt atg ctc cag tat ttt gtc cct ctg ggt ttc att ctt atc tgc Leu Phe Met Leu Gln Tyr Phe Val Pro Leu Gly Phe Ile Leu Ile Cys 215	220	225	1506
tac ctg aag atc gtt ctc tgc ctc cga aaa aga act agg cag gtg gac Tyr Leu Lys Ile Val Leu Cys Leu Arg Lys Arg Thr Arg Gln Val Asp 230	235	240	1554
agg aga aag gaa aat aag agc cgt ctc aat gag aac aag agg gta aat Arg Arg Lys Glu Asn Lys Ser Arg Leu Asn Glu Asn Lys Arg Val Asn 245	250	255	1602
gtg atg ttg att tcc atc gta gtg act ttt gga gcc tgc tgg ttg ccc Val Met Leu Ile Ser Ile Val Val Thr Phe Gly Ala Cys Trp Leu Pro 265	270	275	1650
ttg aac att ttc aat gtc atc ttc gac tgg tat cat gag atg ctg atg Leu Asn Ile Phe Asn Val Ile Phe Asp Trp Tyr His Glu Met Leu Met			1698

	280	285	290	
agc tgc cac cac gac ctg gta ttt gta gtt tgc cac ttg att gct atg Ser Cys His His Asp Leu Val Phe Val Val Cys His Leu Ile Ala Met	295	300	305	1746
gtt tct act tgc ata aat cct ctc ttt tat gga ttt ctc aac aaa aac Val Ser Thr Cys Ile Asn Pro Leu Phe Tyr Gly Phe Leu Asn Lys Asn	310	315	320	1794
ttc cag aag gat cta atg atg ctt att cac cac tgt tgg tgt ggt gaa Phe Gln Lys Asp Leu Met Met Leu Ile His His Cys Trp Cys Gly Glu	325	330	335	1842
cct cag gaa agt tat gaa aat att gcc atg tct act atg cac aca gat Pro Gln Glu Ser Tyr Glu Asn Ile Ala Met Ser Thr Met His Thr Asp	345	350	355	1890
gaa tcc aag gga tca tta aaa ctg gct cac ata cca aca ggc ata tag Glu Ser Lys Gly Ser Leu Lys Leu Ala His Ile Pro Thr Gly Ile	360	365	370	1938
aaactggtaa gcaaaatcaa agcccttctg ttatgaaaga aagagaagaa atagtatgga atagggcaag gtgcagagga agccagactt aaacacataa tatctttggg cccagtttg				1998
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Leu Ala Ile Leu Leu Leu Ile Ala Tyr Thr Val Ile Leu Ile Met  
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Gly Ile Phe Gly Asn Leu Ser Leu Ile Ile Ile Phe Lys Lys Gln  
50               55               60

Arg Glu Ala Gln Asn Val Thr Asn Ile Leu Ile Ala Asn Leu Ser Leu  
65               70               75               80

Ser Asp Ile Leu Val Cys Val Met Cys Ile Pro Phe Thr Val Ile Tyr  
85 90 95

Thr Leu Met Asp His Trp Val Phe Gly Asn Thr Met Cys Lys Leu Thr  
100 105 110

Ser Tyr Val Gln Ser Val Ser Val Ser Ile Phe Ser Leu Val  
115 120 125

Leu Ile Ala Ile Glu Arg Tyr Gln Leu Ile Val Asn Pro Arg Gly Trp  
130 135 140

Lys Pro Arg Val Ala His Ala Tyr Trp Gly Ile Ile Leu Ile Trp Leu  
145 150 155 160

Ile Ser Leu Thr Leu Ser Ile Pro Leu Phe Leu Ser Tyr His Leu Thr  
165 170 175

Asn Glu Pro Phe His Asn Leu Ser Leu Pro Thr Asp Ile Tyr Thr His  
180 185 190

Gln Val Ala Cys Val Glu Ile Trp Pro Ser Lys Leu Asn Gln Leu Leu  
195 200 205

Phe Ser Thr Ser Leu Phe Met Leu Gln Tyr Phe Val Pro Leu Gly Phe  
210 215 220

Ile Leu Ile Cys Tyr Leu Lys Ile Val Leu Cys Leu Arg Lys Arg Thr  
225 230 235 240

Arg Gln Val Asp Arg Arg Lys Glu Asn Lys Ser Arg Leu Asn Glu Asn  
245 250 255

Lys Arg Val Asn Val Met Leu Ile Ser Ile Val Val Thr Phe Gly Ala  
260 265 270

Cys Trp Leu Pro Leu Asn Ile Phe Asn Val Ile Phe Asp Trp Tyr His  
275 280 285

Glu Met Leu Met Ser Cys His His Asp Leu Val Phe Val Val Cys His  
290 295 300

Leu Ile Ala Met Val Ser Thr Cys Ile Asn Pro Leu Phe Tyr Gly Phe  
305 310 315 320

Leu Asn Lys Asn Phe Gln Lys Asp Leu Met Met Leu Ile His His Cys  
325 330 335

Trp Cys Gly Glu Pro Gln Glu Ser Tyr Glu Asn Ile Ala Met Ser Thr  
340 345 350

Met His Thr Asp Glu Ser Lys Gly Ser Leu Lys Leu Ala His Ile Pro  
355 360 365

Thr Gly Ile  
370